

SEQUENCE LISTING

<110> Merck & Co., Inc.
Freedman, Leonard P.
Glantschnig, Helmut
Harada, Shun-ichi
Hess, John W.

<120> CYNOMOLGUS MONKEY DICKKOPF-4,
NUCLEOTIDES ENCODING SAME, AND USES THEREOF

<130> 21351Y

<150> 60/520,569
<151> 2003-11-17

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 675
<212> DNA
<213> MACACA FASCICULARIS

<400> 1
atggcgccgg ccgtcctgct gggactgagc tggctctgct ctccccctggg agctctggtc 60
ctggacttca acaacatca gactctgtct gacctgcttg gggcccgaa gggctcacag 120
tgcctgtctg acacagactg caataccaga aagtctgcc tccagtccta caatgagaag 180
ccgttctgtg ctacatgtcg tgggttgac aggagggtgcc agcgagatgc catgtgctgc 240
cctgggacac tctgcatgaa tgatgtttgt actacgatgg aagacgcAAC cccaaaattg 300
gaaaggcagc ttgatgagca agatggcaca catgcagaag taacaactgg gcacccagtc 360
caggaaaaacc aacccaagag gaagccaagt attaagaaat cacaaggcag gaagggacaa 420
gagggagaaa gttgtctgac aacttttgcac tggccctg gactttgtc tgctgtcat 480
ttttggacga aaatttgtaa gccagtcctt ttggaggggc aggtctgtc caggagaggg 540
cataaaagaca ctgctcaagc tccagaaatc ttccagcgtt gcgactgtgg ccccgacta 600
ctgtgtcgaa gccaaactgac cagcaatca gcatgcac gttacgagt atgcacaaaa 660
atagaaaagc tataa 675

<210> 2
<211> 224
<212> PRT
<213> MACACA FASCICULARIS

<400> 2
Met Ala Ala Ala Val Leu Leu Gly Leu Ser Trp Leu Cys Ser Pro Leu
1 5 10 15
Gly Ala Leu Val Leu Asp Phe Asn Asn Ile Arg Ser Ser Ala Asp Leu
20 25 30
Leu Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys Asn
35 40 45
Thr Arg Lys Phe Cys Leu Gln Ser His Asn Glu Lys Pro Phe Cys Ala
50 55 60
Thr Cys Arg Gly Leu Gln Arg Arg Cys Gln Arg Asp Ala Met Cys Cys
65 70 75 80
Pro Gly Thr Leu Cys Met Asn Asp Val Cys Thr Thr Met Glu Asp Ala
85 90 95

Thr	Pro	Lys	Leu	Glu	Arg	Gln	Leu	Asp	Glu	Gln	Asp	Gly	Thr	His	Ala
							100		105				110		
Glu	Val	Thr	Thr	Gly	His	Pro	Val	Gln	Glu	Asn	Gln	Pro	Lys	Arg	Lys
							115		120			125			
Pro	Ser	Ile	Lys	Lys	Ser	Gln	Gly	Arg	Lys	Gly	Gln	Glu	Gly	Glu	Ser
							130		135			140			
Cys	Leu	Arg	Thr	Phe	Asp	Cys	Gly	Pro	Gly	Leu	Cys	Cys	Ala	Arg	His
							145		150			155			160
Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	Leu	Glu	Gly	Gln	Val	Cys
							165		170			175			
Ser	Arg	Arg	Gly	His	Lys	Asp	Thr	Ala	Gln	Ala	Pro	Glu	Ile	Phe	Gln
							180		185			190			
Arg	Cys	Asp	Cys	Gly	Pro	Gly	Leu	Leu	Cys	Arg	Ser	Gln	Leu	Thr	Ser
							195		200			205			
Asn	Gln	Gln	His	Ala	Arg	Leu	Arg	Val	Cys	Gln	Lys	Ile	Glu	Lys	Leu
							210		215			220			

<210> 3
<211> 841
<212> DNA
<213> HOMO SAPIENS

<400> 3

gcacgagaga	cgacgtgctg	agctgccagc	ttagtggaaag	ctctgctctg	ggtgaggagc	60
agcctcgctt	tggtgacgca	cagtgtctgg	accctccagg	agccccggga	ttgaaggatg	120
gtggcggccg	tcctgctggg	gctgagctgg	ctctgctctc	ccctgggagc	tctggtcctg	180
gacttcaaca	acatcaggag	ctctgctgac	ctgcattgggg	cccgaaaggg	ctcacagtgc	240
ctgtctgaca	cggactgcaa	taccagaaaq	ttctgcctcc	agccccggca	tgagaagccg	300
ttctgtgcta	catgtcgtgg	gttgcggagg	aggtgccagc	gagatgccat	gtgtgcgcct	360
gggacactct	gtgtgaacga	tgttgtact	acgatggaag	atgcaacccc	aatattagaa	420
aggcagctg	atgagcaaga	tggcacacat	gcagaaggaa	caactgggca	cccagtccag	480
gaaaaccaac	ccaaaaggaa	gccaagtatt	aagaaatcac	aaggcaggaa	gggacaagag	540
ggagaaaagg	gtctgagaac	ttttactgt	ggccctggac	tttgctgtgc	tcgtcatttt	600
ttggacgaaaa	ttttaagcc	agtccctttt	gaggacagg	tctgctccag	aagagggcat	660
aaagacactg	ctcaactcc	agaaatctt	cagcgttgcg	actgtggccc	tggactactg	720
tgtcgaagcc	aatttaccag	caatcggcag	catgctcgat	taagagtatg	ccaaaaaaaata	780
gaaaagctat	aaatatttca	aaataaagaa	gaatccacat	tgcaaaaaaaaaa	aaaaaaaaaaa	840
						841

<210> 4
<211> 224
<212> PRT
<213> HOMO SAPIENS

<400> 4

Met	Val	Ala	Ala	Val	Leu	Leu	Gly	Leu	Ser	Trp	Leu	Cys	Ser	Pro	Leu
1							5		10			15			
Gly	Ala	Leu	Val	Leu	Asp	Phe	Asn	Asn	Ile	Arg	Ser	Ser	Ala	Asp	Leu
							20		25			30			
His	Gly	Ala	Arg	Lys	Gly	Ser	Gln	Cys	Leu	Ser	Asp	Thr	Asp	Cys	Asn
							35		40			45			
Thr	Arg	Lys	Phe	Cys	Leu	Gln	Pro	Arg	Asp	Glu	Lys	Pro	Phe	Cys	Ala
							50		55			60			
Thr	Cys	Arg	Gly	Leu	Arg	Arg	Arg	Cys	Gln	Arg	Asp	Ala	Met	Cys	Cys
							65		70			75			80
Pro	Gly	Thr	Leu	Cys	Val	Asn	Asp	Val	Cys	Thr	Thr	Met	Glu	Asp	Ala
							85		90			95			

Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His Ala
 100 105 110
 Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg Lys
 115 120 125
 Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu Ser
 130 135 140
 Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg His
 145 150 155 160
 Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val Cys
 165 170 175
 Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe Gln
 180 185 190
 Arg Cys Asp Cys Gly Pro Gly Leu Leu Cys Arg Ser Gln Leu Thr Ser
 195 200 205
 Asn Arg Gln His Ala Arg Leu Arg Val Cys Gln Lys Ile Glu Lys Leu
 210 215 220

<210> 5
 <211> 221
 <212> PRT
 <213> MUS MUSCULUS

<400> 5
 Met Val Leu Val Thr Leu Leu Gly Leu Ser Trp Phe Cys Ser Pro Leu
 1 5 10 15
 Ala Ala Leu Val Leu Asp Phe Asn Asn Ile Lys Ser Ser Ala Asp Val
 20 25 30
 Gln Gly Ala Gly Lys Gly Ser Leu Cys Ala Ser Asp Arg Asp Cys Ser
 35 40 45
 Glu Gly Lys Phe Cys Leu Ala Phe His Asp Glu Arg Ser Phe Cys Ala
 50 55 60
 Thr Cys Arg Arg Val Arg Arg Arg Cys Gln Arg Ser Ala Val Cys Cys
 65 70 75 80
 Pro Gly Thr Val Cys Val Asn Asp Val Cys Thr Ala Val Glu Asp Thr
 85 90 95
 Arg Pro Val Met Asp Arg Asn Thr Asp Gly Gln Asp Gly Ala Tyr Ala
 100 105 110
 Glu Gly Thr Thr Lys Trp Pro Ala Glu Glu Asn Arg Pro Gln Gly Lys
 115 120 125
 Pro Ser Thr Lys Lys Ser Gln Ser Ser Lys Gly Gln Glu Gly Glu Ser
 130 135 140
 Cys Leu Arg Thr Ser Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg His
 145 150 155 160
 Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Arg Glu Gly Gln Val Cys
 165 170 175
 Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe Gln
 180 185 190
 Arg Cys Asp Cys Gly Pro Gly Leu Thr Cys Arg Ser Gln Val Thr Ser
 195 200 205
 Asn Arg Gln His Ser Arg Leu Arg Val Cys Gln Arg Ile
 210 215 220

<210> 6
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
<223> F2 PRIMER

<400> 6
caggagcccc gggattgaag gatg 24

<210> 7
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> R2 PRIMER

<400> 7
gcaatgtgga ttcttctta ttttgaata tttatagc 38

<210> 8
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> F PRIMER

<400> 8
gcgaattcac catggcgccg gccgtcctgc t 31

<210> 9
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> FF PRIMER

<400> 9
gcgaattcac catggcgccg gccgtcctgc tgggact 37

<210> 10
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> R PRIMER

<400> 10
gcgaattcta gctttctat tttttggcat actcgtaacc gt 42

<210> 11
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> RR PRIMER

<400> 11
gcgaattcta gctttctat ttttggcat actcgtaacc gtgcatg 47

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Fseq PRIMER

<400> 12
gggacactct gcatgaatga tg 22

<210> 13
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Rseq PRIMER

<400> 13
tgccatcttg ctcatcaagc t 21